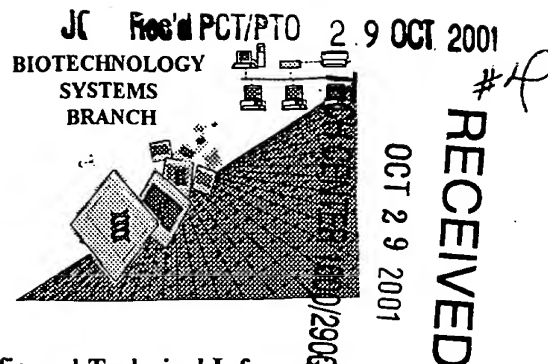


Barbara  
Campbell

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/889,182  
Source: 1600 REISH  
Date Processed by STIC: 10/22/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1600

## RAW SEQUENCE LISTING

DATE: 10/22/2001

PATENT APPLICATION: US/09/889,182

TIME: 12:13:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\10222001\I889182.raw

W--> 1 SEQUENZPROTOKOLL *delete*

4 <110> APPLICANT: Deutsches Krebsforschungszentrum

6 <120> TITLE OF INVENTION: Selektion von monoklonalen Antikörpern

8 <130> FILE REFERENCE: K 2779

OK-> 10 <140> CURRENT APPLICATION NUMBER: US/09/889,182

11 <141> CURRENT FILING DATE: 2000-01-11

13 <150> PRIOR APPLICATION NUMBER: DE 199 00 635.0-41

14 <151> PRIOR FILING DATE: 1999-01-11

16 <160> NUMBER OF SEQ ID NOS: 6

18 <170> SOFTWARE: PatentIn Ver. 2.1.

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 5732

23 <212> TYPE: DNA

24 <213> ORGANISM: knstliche Sequenz

26 <220> FEATURE:

27 <221> NAME/KEY: CDS

28 <222> LOCATION: (737) ... (1420)

29 <223> OTHER INFORMATION: Beschreibung der knstlichen Sequenz: Antikörper-Bindeprotein

32 <400> SEQUENCE: 1

35	gcgcgcgttg	acattgatta	ttgactagtt	attaatagta	atcaattacg	gggtcattag	60	
37	ttcatagccc	atatatggag	ttccgcgtta	cataacttac	ggtaaatggc	ccgcctggct	120	
39	gaccgcacca	cgacccccgc	ccattgacgt	caataatgac	gtatgttccc	atagtaacgc	180	
41	caatagggac	tttccattga	cgtcaatggg	tggactat	acggtaaaact	gcccacttgg	240	
43	cagtacatca	agtgatcat	atgccaagta	cgccccctat	tgacgtcaat	gacggtaaat	300	
45	ggccccgctg	gcattatgcc	cagtacatga	ccttatggga	ctttcctact	tggcagtaca	360	
47	tctacgtatt	agtcacgct	attaccatgg	tgatgcgggt	ttggcagtag	atcaatgggc	420	
49	gtggatagcg	gtttgactca	cggggatttc	caagtcctca	ccccattgac	gtcaatggga	480	
51	gtttgttttg	gcacaaaat	caacgggact	ttccaaaatg	tcgtaaacaac	tccgccccat	540	
53	tgacgcaaat	ggcggttagg	cgtgtacggt	gggaggtcta	tataagcaga	gctctctggc	600	
55	taactagaga	acccactgct	tactggctta	tcgaaattaa	tacgactcac	tatagggaga	660	
57	cccaagcttg	gtaccgagct	cggatccact	agtaacggcc	gccagtgtgc	tggatttcgg	720	
59	cttggggata	tccacc atg	gag aca	gac aca	ctc ctg	cta tgg gta	769	
60	Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu							
61	1	5	10					
63	ctg ctc	tgg gtt	cca ggt	tcc act	ggt gac	tat cca	tat gat gtt cca	817
64	Leu Leu	Trp Val	Pro Gly	Ser Thr	Gly Asp	Tyr Pro	Tyr Asp Val Pro	
65	15	20	25					
67	gat tat	gct ggg	gcc caa	aag ccc	gag gtg	atc gat	gcc agc gag ctg	865
68	Asp Tyr	Ala Gly	Ala Gln	Lys Pro	Glu Val	Ile Asp	Ala Ser Glu Leu	
69	30	35	40					
71	acc ccc	gcc gtg	acc acc	tac aag	cta gtg	atc aac	ggc aag acc ctg	913
72	Thr Pro	Ala Val	Thr Thr	Lys Lys	Leu Val	Ile Asn	Gly Lys Thr Leu	
73	45	50	55					
75	aag ggc	gag acc	acc acc	gag gcc	gtg gac	gcc gcc	acc gcg gag aag	961
76	Lys Gly	Glu Thr	Thr Thr	Glu Ala	Val Asp	Ala Ala	Thr Ala Glu Lys	
77	60	65	70	75				
79	gtg ttc	aaa caa	tac gct	aat gac	aac ggg	gtc gac	ggc gag tgg act	1009

*all U.S.  
Applications  
must be in  
English*

**Does Not Comply  
Corrected Diskette Needed**

*pp 1,4*

## RAW SEQUENCE LISTING

DATE: 10/22/2001

PATENT APPLICATION: US/09/889,182

TIME: 12:13:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\10222001\I889182.raw

```

80 Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr
81          80          85          90
83 tac gac gac gcc acc aag acc ttc acc gtg acc gag aag ccc gag gtg      1057
84 Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val
85          95          100          105
87 atc gat gcc agc gag ctg acc ccc gcc gtg acc acc tac aag cta gtg      1105
88 Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val
89          110          115          120
91 atc aac ggc aag acc ctg aag ggc gag acc acc acc gag gcc gtg gac      1153
92 Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp
93          125          130          135
95 gcc gcc acc gcg gag aag gtg ttc aaa caa tac gct aat gac aac ggg      1201
96 Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly
97 140          145          150          155
99 gtc gac ggc gag tgg act tac gac gac gcc acc aag acc ttc acc gtg      1249
100 Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val
101          160          165          170
103 acc gag gcg gcc gca gaa caa aaa ctc atc tca gaa gag gat ctg aat      1297
104 Thr Glu Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
105          175          180          185
107 ggg gcc gtc gac gga caa aac gac acc agc caa acc agc agc ccc tca      1345
108 Gly Ala Val Asp Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
109          190          195          200
111 gca tcc agc aac ata agc gga ggc att ttc ctt ttc ttc gtg gcc aat      1393
112 Ala Ser Ser Asn Ile Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn
113          205          210          215
115 gcc ata atc cac ctc ttc tgc ttc agt tgaggtgaca cgtctagagc      1440
116 Ala Ile Ile His Leu Phe Cys Phe Ser
117 220          225
119 tattctatag tgtcacctaa atgctagagc tcgctgatca gcctcgactg tgccttctag      1500
121 ttgccagcca tctgttgttt gcccctcccc cgtgccttcc ttgacctgga aaggtgccac      1560
123 tcccactgtc ctttcctaat aaaatgagga aattgcatcg cattgtctga gtaggtgtca      1620
125 ttctattctg gggggtgggg tggggcagga cagcaagggg gaggattggg aagacaatag      1680
127 caggcatgct ggggatgcgg tgggctctat ggcttctgag gcggaaagaa ccagtggcgg      1740
129 taatacgggt atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc      1800
131 agcaaaaaggc caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggtccgcc      1860
133 cccctgacga gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac      1920
136 tataaagata ccaggcgttt cccctggaa gctccctcgt gcgctctcct gttccgacct      1980
138 tgccgcttac cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata      2040
140 gctcacgctg taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc      2100
142 acgaaccccc cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca      2160
144 acccggttaag acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag      2220
146 cgaggatagt aggcggtgct acagagtctt tgaagtgggt gcctaactac ggctacacta      2280
148 gaaggacagt atttggatat tgcgctctgc tgaagccagt taccttcgga aaaagagttg      2340
150 gtagctcttg atccggcaaa caaaccaccg ctggtagcgg tgggtttttt gtttgcaagc      2400
152 agcagattac gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggg      2460
154 ctgacgctca gtggaacgaa aactcacggt aagggatttt ggtcatgaga ttatcaaaaa      2520
156 ggatcttcac ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat      2580
158 atgagtaacc tgaggctatg gcagggcctg ccgccccgac gttggctgcg agccctgggc      2640

```

## RAW SEQUENCE LISTING

DATE: 10/22/2001

PATENT APPLICATION: US/09/889,182

TIME: 12:13:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\10222001\I889182.raw

160	cttcacccga	acttgggggg	tggggtgggg	aaaaggaaga	aacgcgggcg	tattggcccc	2700
162	aatgggggtct	cgggtgggga	tcgacagagt	gccagccctg	ggaccgaacc	ccgcgtttat	2760
164	gaacaaacga	cccaacaccg	tgcgttttat	tctgtctttt	tattgccgtc	atagcgcggg	2820
166	ttccttcggg	tattgtctcc	ttccgtgttt	cagttagcct	ccccctaggg	tgggcgaaga	2880
168	actccagcat	gagatccccg	cgctggagga	tcattccagcc	ggcgccccg	aaaacgattc	2940
170	cgaagcccaa	cctttcatag	aaggcgggcg	tggaatcgaa	atctcgtgat	ggcaggtttg	3000
172	gcgtcgcttg	gtcggtcatt	tcgaacccca	gagtcgccgt	cagaagaact	cgtaagaag	3060
174	gcgatagaag	gcgatgcgct	gcgaatcggg	agcggcgata	ccgtaaagca	cgaggaagcg	3120
176	gtcagcccat	tcgcccga	gctcttcagc	aatatcacgg	gtagccaacg	ctatgtcctg	3180
178	atagcgggtcc	gccacaccca	gccggccaca	gtcgatgaat	ccagaaaagc	ggccattttc	3240
180	caccatgata	ttcggaagc	aggcatcgcc	atgggtcacg	acgagatcct	cgccgtcggg	3300
182	ctgcgtcgcc	ttagcctgg	cgaacagtcc	ggctggcgcg	agccctgat	gctcttgatc	3360
184	atcctgatcg	acaagaccgg	cttccatccg	agtaacgtct	cgctcgatgc	gatgtttcgc	3420
186	ttggtggctg	aatgggcagg	tagccggatc	aagcgtatgc	agccgcgcga	ttgcatcagc	3480
188	catgatggat	actttctcgg	caggagcaag	gtgagatgac	aggagatcct	gccccggcac	3540
190	ttcgcccaat	agcagccagt	cccttcccgc	ttcagtgaca	acgtcgagca	cagctgcgca	3600
192	aggaacgccc	gtcgtggcca	gccacgatag	ccgcgctgcc	tcgtcttgca	gttcattcag	3660
194	ggcaccggac	aggtcggtct	tgacaaaaag	aaccgggcgc	ccctgcgctg	acagccggaa	3720
196	cacggcgcca	tcagagcagc	cgattgtctg	ttgtgccag	tcatagccga	atagcctctc	3780
198	cacccaagcg	gccggagaac	ctgcgtgcaa	tcctcttgt	tcaatcatgc	gaaacgatcc	3840
200	tcactctgtc	tcttgatcga	tctttgcaaa	agcctaggcc	tccaaaaaag	cctcctcact	3900
202	acttctggaa	tagctcagag	gccgaggagg	cggcctcggc	ctctgcataa	ataaaaaaaa	3960
205	ttagtcagcc	atggggcgga	gaatgggcgg	aactgggcgg	agttaggggc	gggatgggcg	4020
207	gagttagggg	cgggactatg	gttgctgact	aattgagatg	catgctttgc	atacttctgc	4080
209	ctgctgggga	gcttggggac	tttccacacc	tggttgctga	ctaattgaga	tgcatgcttt	4140
211	gcatacttct	gctgtcgtgg	gagcctgggg	actttccaca	ccctaactga	cacacattcc	4200
213	acagctggtt	ctttccgcct	caggactctt	cccttttcaa	taaatcaatc	taaaagtatat	4260
215	atgagtaaac	ttggtctgac	agttaccaat	gcttaatcag	tgaggcacct	atctcagcga	4320
217	tctgtctatt	tcgttcatcc	atagttgcct	gactccccgt	cgtgtagata	actacgatac	4380
219	gggagggctt	accatctggc	cccagtgtcg	caatgatacc	gcgagaccca	cgctcaccgg	4440
221	ctccagattt	atcagcaata	aaccagccag	ccggaagggc	cgagcgagca	agtggctcctg	4500
223	caactttatc	cgctccatc	cagtctatta	attgttgccg	ggaagctaga	gtaagtgtt	4560
225	cgccagttaa	tagtttgccg	aacgttggtg	ccattgctac	aggcatcggtg	gtgtcacgct	4620
227	cgtcgttttg	tatggcttca	ttcagctccg	gttcccaacg	atcaaggcga	gttacatgat	4680
229	cccccatggt	gtgcaaaaaa	gcggttagct	ccttcggtcc	tccgatcggt	gtcagaagta	4740
231	agttggccgc	agtgttatca	ctcatggtta	tggcagcact	gcataattct	cttactgtca	4800
233	tgccatccgt	aagatgcttt	tctgtgactg	gtgagtactc	aaccaagtca	ttctgagaat	4860
235	agtgtatcg	gcgaccgagt	tgctcttgcc	cggcgccaat	acgggataat	accgcgccac	4920
237	atagcagaac	tttaaaagt	ctcatcattg	gaaaacgttc	ttcggggcga	aaactctcaa	4980
239	ggatcttacc	gctgttgaga	tccagttcga	tgtaacccac	tcgtgcaccc	aactgatctt	5040
241	cagcatcttt	tactttcacc	agcgtttctg	ggtgagcaaa	aacaggaagg	caaaatgcg	5100
243	caaaaaagg	aataaggcg	acacggaaat	gttgaatact	catactcttc	ctttttcaat	5160
245	attattgaag	catttatcag	ggttattgtc	tcatgagcgg	atacatattt	gaatgtattt	5220
247	agaaaaataa	acaaatagg	gttccgcgca	catttccccc	aaaagtgcc	cctgacgcgc	5280
249	cctgtagcgg	cgcattaagc	gcggcgggtg	tgggtggtac	gcgcagcggtg	accgctacac	5340
251	ttgccagcgc	cctagcgccc	gtcctttctg	ctttcttccc	ttcctttctc	gccacgttcg	5400
253	ccggctttcc	ccgtcaagct	ctaaatcggg	ggctcccttt	agggttccga	tttagtgctt	5460
255	tacggcacct	cgaccccaaa	aaacttgatt	aggggtgatg	ttcacgtagt	gggccatcgc	5520
257	cctgatagac	ggtttttcgc	cctttgacgt	tggagtcac	gttctttaat	agtggaactct	5580

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/889,182

DATE: 10/22/2001

TIME: 12:13:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\10222001\I889182.raw

259 tgttccaaac tggacaaca ctcaacccta tctcgggtcta ttcttttgat ttataagggg 5640  
 261 ttttgccgat ttgggcctat tgggttaaaaa atgagctgat ttaacaaaaa tttaacgcga 5700  
 263 attttaacaa aatattaacg cttacaattt ac 5732  
 267 <210> SEQ ID NO: 2  
 268 <211> LENGTH: 228  
 269 <212> TYPE: PRT  
 270 <213> ORGANISM: knstliche Sequenz *insert this mandatory numeric identifier whenever C2217, C2227, or C2237*  
 272 <223> OTHER INFORMATION: Beschreibung der knstlichen Sequenz: Antikrper-Bindeprotein *is shown*  
 274 <400> SEQUENCE: 2  
 277 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 278 1 5 10 15  
 280 Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala  
 281 20 25 30  
 283 Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr  
 284 35 40 45  
 286 Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr  
 287 50 55 60  
 289 Thr Glu Ala Val Asp Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr  
 290 65 70 75 80  
 292 Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr  
 293 85 90 95  
 295 Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu  
 296 100 105 110  
 298 Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr  
 299 115 120 125  
 301 Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Thr Ala Glu  
 302 130 135 140  
 304 Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp  
 305 145 150 155 160  
 307 Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Ala Ala Ala  
 308 165 170 175  
 310 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Val Asp Gly  
 311 180 185 190  
 313 Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala Ser Ser Asn Ile  
 314 195 200 205  
 316 Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu  
 317 210 215 220  
 319 Phe Cys Phe Ser  
 320 225  
 324 <210> SEQ ID NO: 3  
 325 <211> LENGTH: 6094  
 326 <212> TYPE: DNA  
 327 <213> ORGANISM: knstliche Sequenz  
 329 <220> FEATURE:  
 330 <221> NAME/KEY: CDS  
 331 <222> LOCATION: (682) ... (1782)  
 332 <223> OTHER INFORMATION: Beschreibung der knstlichen Sequenz: Antikrper-Bindeprotein  
 334 <400> SEQUENCE: 3  
 337 ggcgcggttg acattgatta ttgactagtt attaatagta atcaattacg gggtcattag 60

The types of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

## RAW SEQUENCE LISTING

DATE: 10/22/2001

PATENT APPLICATION: US/09/889,182

TIME: 12:13:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\10222001\I889182.raw

```

339 ttcatagccc atatattggag ttccgcgtta cataacttac ggtaaattgc ccgcctggct 120
341 gaccgcccac cgacccccgc ccattgacgt caataatgac gtatgttccc atagtaacgc 180
343 caatagggac tttccattga cgtcaatggg tggactatgt acggtaaact gccacttgg 240
345 cagtacatca agtgtatcat atgccaaagta cgtcccttat tgacgtcaat gacggtaaat 300
347 ggcccgccgt gcattatgcc cagtacatga ccttatggga ctttctact tggcagtaca 360
349 tctacgtatt agtcacgtct attaccatgg tgatgcggtt ttggcagtac atcaatgggc 420
351 gtggatagcg gtttgactca cggggatttc caagtctcca cccattgac gtcaatggga 480
353 gtttgttttg gcacaaaaat caacgggact ttccaaaatg tcgtaacaac tccgccccat 540
355 tgacgcaaat gggcggtagg cgtgtacggt gggagggtcta tataagcaga gctctctggc 600
357 taactagaga acccaactgct tactggctta tcgaaattaa tacgactcac tatagggaga 660
359 cccaagcttg gtaccggtgc g atg gca ccc tgc atg ctg ctc ctg ctg ttg 711
360 Met Ala Pro Cys Met Leu Leu Leu Leu Leu
361 1 5 10
364 gcg gcc gcc ctg gcc ccg act cag acc cgc gcg ggg gcc caa aag gag 759
365 Ala Ala Ala Leu Ala Pro Thr Gln Thr Arg Ala Gly Ala Gln Lys Glu
366 15 20 25
368 aag acc ccc gag gag ccc aag gag gag gtg acc atc aag gcc aac ctg 807
369 Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu
370 30 35 40
372 atc tac gcc gac ggc aag acc cag acc gcc gag ttc aag ggc acc ttc 855
373 Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe
374 45 50 55
376 gag gag gcc acc gcg gag gcc tac cgc tac gcc gac gcc ctg aag aag 903
377 Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys
378 60 65 70
380 gac aac ggc gag tac acc gtg gac gtg gcc gac aag ggc tac acc ctg 951
381 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu
382 75 80 85 90
385 aac atc aag ttc gcc ggc aag gag aag acc ccc gag gag ccc aag gag 999
386 Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu
387 95 100 105
389 gag gtg acc atc aag gcc aac ctg atc tac gcc gac ggc aag acc cag 1047
390 Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln
391 110 115 120
393 acc gcc gag ttc aag ggc acc ttc gag gag gcc acc gcg gag gcc tac 1095
394 Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr
395 125 130 135
397 cgc tac gcc gac gcc ctg aag aag gac aac ggc gag tac acc gtg gac 1143
398 Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp
399 140 145 150
401 gtg gcc gac aag ggc tac acc ctg aac atc aag ttc gcc ggc aag gag 1191
402 Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu
403 155 160 165 170
406 aag acc ccc gag gag ccc aag gag gag gtg acc atc aag gcc aac ctg 1239
407 Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu
408 175 180 185
410 atc tac gcc gac ggc aag acc cag acc gcc gag ttc aag ggc acc ttc 1287
411 Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe
412 190 195 200

```

VERIFICATION SUMMARY

DATE: 10/22/2001

PATENT APPLICATION: US/09/889,182

TIME: 12:13:25

Input Set : A:\ES.txt

Output Set: N:\CRF3\10222001\I889182.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
 L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
 L:433 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:437 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:441 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:445 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:738 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:742 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:746 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:750 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:754 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:758 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:762 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:766 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:770 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:774 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:778 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:782 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:786 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5